UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

KD

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/009,802	01/20/98	MCCARTHY	~~ME1-008-1~~ ME1-008

000959
LAHIVE & COCKFIELD
28 STATE STREET
BOSTON MA 02109

HM12/0928

DOCKETED

EXAMINER	
YUCEL, I	
ART UNIT	**PAPER NUMBER**
1636	6

Oct. 28, 1999* - RESTRICTION REQUIREMENT

DATE MAILED: 09/28/99

Mar. 28, 2000 - ESP/5 MOS

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

Please see attached

2 - Mail Copy

Office Action Summary

Application No.	Applicant(s)
09/009,802	McCarthy
Examiner	**Group Art Unit**
Remy Yucel	1636

☒ Responsive to communication(s) filed on *Oct 9, 1998* .

☐ This action is **FINAL.**

☐ Since this application is in condition for allowance except for formal matters, **prosecution as to the merits is closed** in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11; 453 O.G. 213.

A shortened statutory period for response to this action is set to expire *one* month(s), or thirty days, whichever is longer, from the mailing date of this communication. Failure to respond within the period for response will cause the application to become abandoned. (35 U.S.C. § 133). Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

Disposition of Claims

☒ Claim(s) *1-60* is/are pending in the application.

Of the above, claim(s) _____ is/are withdrawn from consideration.

☐ Claim(s) _____ is/are allowed.

☐ Claim(s) _____ is/are rejected.

☐ Claim(s) _____ is/are objected to.

☒ Claims *1-60* are subject to restriction or election requirement.

Application Papers

☐ See the attached Notice of Draftsperson's Patent Drawing Review, PTO-948.

☐ The drawing(s) filed on _____ is/are objected to by the Examiner.

☐ The proposed drawing correction, filed on _____ is ☐approved ☐disapproved.

☐ The specification is objected to by the Examiner.

☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. § 119

☐ Acknowledgement is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d).

☐ All ☐ Some* ☐ None of the CERTIFIED copies of the priority documents have been

☐ received.

☐ received in Application No. (Series Code/Serial Number) _____ .

☐ received in this national stage application from the International Bureau (PCT Rule 17.2(a)).

*Certified copies not received: _____ .

☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. § 119(e).

Attachment(s)

☐ Notice of References Cited, PTO-892

☐ Information Disclosure Statement(s), PTO-1449, Paper No(s). _____

☐ Interview Summary, PTO-413

☐ Notice of Draftsperson's Patent Drawing Review, PTO-948

☐ Notice of Informal Patent Application, PTO-152

☒ Notice to Comply .... Sequence Disclosures + Error Report

--- SEE OFFICE ACTION ON THE FOLLOWING PAGES ---

DETAILED ACTION

Claims 1-60 are pending in the application.

Specification

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures and the Raw Sequence Listing Error Report.

Since the response appears to be **bona fide**, but through an apparent oversight or inadvertence failed to provide a complete response, applicant is required to complete the response within a time limit of one (1) month from the date of this letter, 37 CFR 1.135(c).

NO EXTENSION OF THIS TIME LIMIT MAY BE GRANTED UNDER EITHER 37 C.F.R. 1.136(a) OR (b), BUT THE STATUTORY PERIOD FOR RESPONSE SET FOR THIS COMMUNICATION MAILED MAY BE EXTENDED UP TO A MAXIMUM OF SIX (6) MONTHS UNDER 37 CFR 1.136.

Election/Restriction

Restriction to one of the following inventions is required under 35 U.S.C. 121:

I. Claims 1-17, drawn to nucleic acids, vectors, host cells and methods of producing CRSP protein, classifiable in class 536, subclass 23.1 and class 435, subclasses 325 and 69.1.

II. Claims 18 and 19, drawn to a transgenic animal comprising a transgene encoding CRSP, classifiable in class 800, subclass 8.

III. Claims 20-31, drawn to isolated CRSP proteins and fusion proteins, classifiable in class 530, subclass 350.

IV. Claims 32-34, drawn to antibodies which specifically bind CRSP, classifiable in class 424, subclass 130.

V. Claim 38, drawn to a method of modulating a cell-associated activity by stimulating CRSP protein activity or expression classifiable in class 435, subclass 4.

VI. Claim 40, drawn to a method of modulating a cell-associated activity by inhibiting CRSP protein activity or expression, using anti-sense, classifiable in class 536, subclass 24.5.

VII. Claim 41, drawn to a method of modulating a cell-associated activity by inhibiting CRSP protein activity or expression, using an antibody, classifiable in class 424, subclass 130.

VIII. Claim 44, drawn to a method of treating a subject with a small molecule, classifiable in class 514, subclass 1.

IX. Claim 45, drawn to a method of treating a subject with a protein, classifiable in class 514, subclass 2.

X. Claim 46, drawn to a method of treating a subject with a nucleic acid, classifiable in class 514, subclass 44.

XI. Claims 50, 51 and 55, drawn to method of detecting for the presence of CRSP activity using nucleic acid, classifiable in class 435, subclass 6.

XII. Claims 52, 53 and 56, drawn to method of detecting for the presence of CRSP activity using antibodies, classifiable in class 435, subclass 7.1.

XIII. Claim 59, drawn to an assay for detecting a genetic alteration in a cell, classifiable in class 435, subclass 6.

XIV. Claim 60, drawn to an assay for detecting a genetic alteration in a cell, classifiable in class 435, subclass 91.

Claims 37 and 42 are generic to groups V, VI and VII.

Claim 39 is generic to groups VI and VII.

Claims 43, 47 and 48 are generic to groups VIII, IX and X.

Claims 49, 54, and 57 are generic to groups XI and XII.

Claim 58 is generic to groups XIII and XIV.

Election of any one of the groups listed immediately above will result in examination of the corresponding generic claim(s).

The inventions are distinct, each from the other because of the following reasons:

Inventions of groups I-IV are distinct. Inventions are unrelated if it can be shown that they are not disclosed as capable of use together and they have different modes of operation, different functions, or different effects (MPEP § 806.04, MPEP § 808.01). In the instant case the different groups are drawn to chemically and biologically distinct products which are not disclosed as capable of use together. For example, the nucleic acids of group I are distinct from proteins and antibodies and transgenic animals of groups II-IV.

Inventions V-XIV are distinct. Inventions are unrelated if it can be shown that they are not disclosed as capable of use together and they have different modes of operation, different functions, or different effects (MPEP § 806.04, MPEP § 808.01). In the instant case the different groups are drawn to distinct methods that do not contain the same steps, the methods are not disclosed as capable of use together and the methods all have different functions. For example, the method of claim V is a method of modulating a cell-associated activity by stimulating CRSP protein activity or expression; whereas the methods of groups VI and VII are drawn to methods of modulating a cell-associated activity by inhibiting CRSP protein activity or expression by using chemically distinct products, specifically, antisense nucleic acids and antibodies. Groups VIII-X are drawn to methods of treating an individual and have different functions and effects from the methods of V-VII. Groups XI and XII are drawn to methods of detecting CRSP protein activity in a biological sample and have different functions and effects from methods of modulating a cellular activity (V-VII) and methods of treating an individual (VIII-X). Finally, groups XIII and

XIV are drawn to diagnostic methods to detect a genetic alteration and have different functions and effects from methods of modulating a cellular activity (V-VII), methods of treating an individual (VIII-X) and methods of detecting CRSP protein activity in a biological sample (XI and XII).

The product of group I may be used in the distinct methods of groups V, VI, X, XI, XIII and XIV. The product of group II is not disclosed as capable of use with any of the methods of groups V-XIV. The product of group III may be used in the distinct methods of groups VIII and IX and the product of group IV may be used in the distinct methods of groups VII and XII. The inventions can be shown to be distinct if either or both of the following can be shown: (1) the process for using the product as claimed can be practiced with another materially different product or (2) the product as claimed can be used in a materially different process of using that product (MPEP § 806.05(h)). In the instant case the same product may be used in materially different processes such as methods of modulating a cellular activity and methods of diagnosing a genetic alteration (both are performed with the product of group I). Conversely, a method for modulating a cellular activity may be performed with antisense molecules (group I) or with an antibody or a protein (groups IV and III, respectively). Thus, the instant inventions are distinct.

Because these inventions are distinct for the reasons given above and have acquired a separate status in the art because of their recognized divergent subject matter and as shown by

their different classification and because the searches required for the groups are not coextensive, restriction for examination purposes as indicated is proper.

Applicant is advised that the reply to this requirement to be complete must include an election of the invention to be examined even though the requirement be traversed (37 CFR 1.143).

Conclusion

Certain papers related to this application may be submitted to Art Unit 1636 by facsimile transmission. The faxing of such papers must conform with the notices published in the Official Gazette, 1156 OG 61 (November 16, 1993) and 1157 OG 94 (December 28, 1993) (see 37 CFR § 1.6 (d)). The Group 1600 FAX numbers are (703) 308-4242 or (703) 305-3014. Unofficial faxes may be sent to the examiner at (703) 305-7939. NOTE: If applicant *does* submit a paper by fax, the original signed copy should be retained by Applicant or Applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED so as to avoid the processing of duplicate papers in the Office.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Remy Yucel, Ph. D. whose telephone number is (703) 305-1998. The examiner can normally be reached on Monday through Fridays from 8:30 am to 5:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. George Elliott can be reached at (703) 308-4003.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

REMY YUCEL, PH.D
PATENT EXAMINER

Remy Yucel, Ph. D.
September 27, 1999

Application No. 09/009802

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☑ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

☑ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☐ 7.

Other: _____

Applicant must provide:

☑ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☑ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

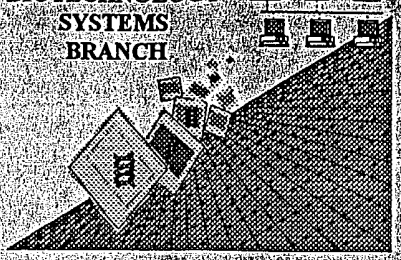
For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.

Rejected

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/009802A

Art Unit / Team No.: 1636

Date Processed by STIC: 9/13/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/009,802A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 ____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 ____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 ____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 ____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: **(2) INFORMATION FOR SEQ ID NO:X:** **(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS") **(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:** **This sequence is intentionally skipped** Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. **<210> sequence Id number** **<400> sequence Id number** **000**
J	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
____	Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.
____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
____	PatentIn ver. 2.0 "bug"	**Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/009,802A

DATE: 09/13/1999
TIME: 12:48:44

Input Set: I009802A.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

see pp. 5, 12

Does Not Comply
Corrected Diskette Needed

<110> APPLICANT: McCarthy, Sean A.
<120> TITLE OF INVENTION: NOVEL CRSP PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREFOR
<130> FILE REFERENCE: MEI-008
<140> CURRENT APPLICATION NUMBER: US/09/009,802A
<141> CURRENT FILING DATE: 1998-01-20
<150> EARLIER APPLICATION NUMBER: 08/842,898
<151> EARLIER FILING DATE: 1997-04-17
<150> EARLIER APPLICATION NUMBER: 60/071,589
<151> EARLIER FILING DATE: 1998-01-15
<160> NUMBER OF SEQ ID NOS: 19
<170> SOFTWARE: PatentIn Ver. 2.0
<210> SEQ ID NO 1
<211> LENGTH: 2479
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (38)..(1087)
<400> SEQUENCE: 1

```
ggcacgaggg ggcggcggct gcgggcgcag agcggag atg cag cgg ctt ggg gcc  55
                                          Met Gln Arg Leu Gly Ala
                                            1               5

acc ctg ctg tgc ctg ctg ctg gcg gcg gcg gtc ccc acg gcc ccc gcg  103
Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala Val Pro Thr Ala Pro Ala
            10                  15                  20

ccc gct ccg acg gcg acc tcg gct cca gtc aag ccc ggc ccg gct ctc  151
Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu
        25                  30                  35

agc tac ccg cag gag gag gcc acc ctc aat gag atg ttc cgc gag gtt  199
Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val
    40                  45                  50

gag gaa ctg atg gag gac acg cag cac aaa ttg cgc agc gcg gtg gaa  247
Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu
55                  60                  65                  70

gag atg gag gca gaa gaa gct gct gct aaa gca tca tca gaa gtg aac  295
Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Ala Ser Ser Glu Val Asn
                75                  80                  85

ctg gca aac tta cct ccc agc tat cac aat gag acc aac aca gac acg  343
Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr
            90                  95                  100

aac gtt gga aat aat acc atc cat gtg cac cga gaa att cac aag ata  391
Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile
        105                 110                 115
```

```
45          acc aac aac cag act gga caa atg gtc ttt tca gag aca gtt atc aca   439
46          Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr
47              120                 125                 130
48          tct gtg gga gac gaa gaa ggc aga agg agc cac gag tgc atc atc gac   487
49          Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp
50          135                 140                 145                 150
51          gag gac tgt ggg ccc agc atg tac tgc cag ttt gcc agc ttc cag tac   535
52          Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr
53                          155                 160                 165
54          acc tgc cag cca tgc cgg ggc cag agg atg ctc tgc acc cgg gac agt   583
55          Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser
56                      170                 175                 180
57          gag tgc tgt gga gac cag ctg tgt gtc tgg ggt cac tgc acc aaa atg   631
58          Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met
59                  185                 190                 195
60          gcc acc agg ggc agc aat ggg acc atc tgt gac aac cag agg gac tgc   679
61          Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys
62              200                 205                 210
63          cag ccg ggg ctg tgc tgt gcc ttc cag aga ggc ctg ctg ttc cct gtg   727
64          Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val
65          215                 220                 225                 230
66          tgc aca ccc ctg ccc gtg gag ggc gag ctt tgc cat gac ccc gcc agc   775
67          Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser
68                          235                 240                 245
69          cgg ctt ctg gac ctc atc acc tgg gag cta gag cct gat gga gcc ttg   823
70          Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu
71                      250                 255                 260
72          gac cga tgc cct tgt gcc agt ggc ctc ctc tgc cag ccc cac agc cac   871
73          Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His
74                  265                 270                 275
75          agc ctg gtg tat gtg tgc aag ccg acc ttc gtg ggg agc cgt gac caa   919
76          Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln
77              280                 285                 290
78          gat ggg gag atc ctg ctg ccc aga gag gtc ccc gat gag tat gaa gtt   967
79          Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val
80          295                 300                 305                 310
81          ggc agc ttc atg gag gag gtg cgc cag gag ctg gag gac ctg gag agg   1015
82          Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg
83                          315                 320                 325
84          agc ctg act gaa gag atg gcg ctg agg gag cct gcg gct gcc gcc gct   1063
85          Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala Ala
86                      330                 335                 340
87          gca ctg ctg gga agg gaa gag att tagatctgga ccaggctgtg ggtagatgtg   1117
88          Ala Leu Leu Gly Arg Glu Glu Ile
89                  345                 350
-> 90       caatagaaat agctaattta tttccccagg tgtgtgcttt aagcgtgggc tgaccaggct 1177
91          tcttcctaca tcttcttccc agtaagtttc ccctctggct tgacagcatg aggtgttgtg 1237
92          catttgttca gctcccccag gctgttctcc aggcttcaca gtctggtgct tgggagagtc 1297
93          aggcagggtt aaactgcagg agcagtttgc cacccctgtc cagattattg gctgctttgc 1357
94          ctctaccagt tggcagacag ccgtttgttc tacatggctt tgataattgt ttgaggggag 1417
```

see item 10 on Error Summary Sheet

```
 95        gagatggaaa caatgtggag tctccctctg attggttttg gggaaatgtg gagaagagtg 1477
 96        ccctgctttg caaacatcaa cctggcaaaa atgcaacaaa tgaattttcc acgcagttct 1537
 97        ttccatgggc ataggtaagc tgtgccttca gctgttgcag atgaaatgtt ctgttcaccc 1597
 98        tgcattacat gtgtttattc atccagcagt gttgctcagc tcctacctct gtgccagggc 1657
 99        agcattttca tatccaagat caattccctc tctcagcaca gcctggggag ggggtcattg 1717
100        ttctcctcgt ccatcaggga tttcagaggc tcagagactg caagctgctt gcccaagtca 1777
101        cacagctagt gaagaccaga gcagtttcat ctggttgtga ctctaagctc agtgctctct 1837
102        ccactacccc acaccagcct tggtgccacc aaaagtgctc cccaaaagga aggagaatgg 1897
103        gatttttctt ttgaggcatg cacatctgga attaaggtca aactaattct cacatccctc 1957
104        taaaagtaaa ctactgttag gaacagcagt gttctcacag tgtggggcag ccgtccttct 2017
105        aatgaagaca atgatattga cactgtccct ctttggcagt tgcattagta actttgaaag 2077
106        gtatatgact gagcgtagca tacaggttaa cctgcagaaa cagtacttag gtaattgtag 2137
107        ggcgaggatt ataaatgaaa tttgcaaaat cacttagcag caactgaaga caattatcaa 2197
108        ccacgtggag aaaatcaaac cgagcagggc tgtgtgaaac atggttgtaa tatgcgactg 2257
109        cgaacactga actctacgcc actccacaaa tgatgttttc aggtgtcatg gactgttgcc 2317
110        accatgtatt catccagagt tcttaaagtt taaagttgca catgattgta taagcatgct 2377
111        ttctttgagt tttaaattat gtataaacat aagttgcatt tagaaatcaa gcataaatca 2437
112        cttcaactgc taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa                    2479
113   <210> SEQ ID NO 2
114   <211> LENGTH: 350
115   <212> TYPE: PRT
116   <213> ORGANISM: Homo sapiens
117   <400> SEQUENCE: 2
118        Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
119          1               5                  10                  15
120        Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
121                     20                  25                  30
122        Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
123                 35                  40                  45
124        Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
125             50                  55                  60
126        Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
127         65                  70                  75                  80
128        Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
129                         85                  90                  95
130        Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
131                     100                 105                 110
132        Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
133                 115                 120                 125
134        Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
135             130                 135                 140
136        His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
137        145                 150                 155                 160
138        Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
139                         165                 170                 175
140        Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
141                     180                 185                 190
142        Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
143                 195                 200                 205
144        Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
```

```
145             210                 215                 220
146         Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
147         225                 230                 235                 240
148         Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
149                         245                 250                 255
150         Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
151                     260                 265                 270
152         Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
153                 275                 280                 285
154         Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
155             290                 295                 300
156         Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
157         305                 310                 315                 320
158         Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
159                         325                 330                 335
160         Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Arg Glu Glu Ile
161                     340                 345                 350
162   <210> SEQ ID NO 3
163   <211> LENGTH: 1050
164   <212> TYPE: DNA
165   <213> ORGANISM: Homo sapiens
166   <220> FEATURE:
167   <221> NAME/KEY: CDS
168   <222> LOCATION: (1)..(1050)
169   <400> SEQUENCE: 3
170         atg cag cgg ctt ggg gcc acc ctg ctg tgc ctg ctg ctg gcg gcg gcg   48
171         Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
172           1               5                  10                  15
173         gtc ccc acg gcc ccc gcg ccc gct ccg acg gcg acc tcg gct cca gtc   96
174         Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
175                     20                  25                  30
176         aag ccc ggc ccg gct ctc agc tac ccg cag gag gag gcc acc ctc aat   144
177         Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
178                 35                  40                  45
179         gag atg ttc cgc gag gtt gag gaa ctg atg gag gac acg cag cac aaa   192
180         Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
181              50                  55                  60
182         ttg cgc agc gcg gtg gaa gag atg gag gca gaa gaa gct gct gct aaa   240
183         Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
184          65                  70                  75                  80
185         gca tca tca gaa gtg aac ctg gca aac tta cct ccc agc tat cac aat   288
186         Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
187                         85                  90                  95
188         gag acc aac aca gac acg aac gtt gga aat aat acc atc cat gtg cac   336
189         Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
190                     100                 105                 110
191         cga gaa att cac aag ata acc aac aac cag act gga caa atg gtc ttt   384
192         Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
193                 115                 120                 125
194         tca gag aca gtt atc aca tct gtg gga gac gaa gaa ggc aga agg agc   432
```

GE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/009,802A

DATE: 09/13/1999
TIME: 12:48:44

Input Set: I009802A.RAW

```
195         Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
196             130                 135                 140
197         cac gag tgc atc atc gac gag gac tgt ggg ccc agc atg tac tgc cag   480
198         His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
199         145                 150                 155                 160
200         ttt gcc agc ttc cag tac acc tgc cag cca tgc cgg ggc cag agg atg   528
201         Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
202                         165                 170                 175
203         ctc tgc acc cgg gac agt gag tgc tgt gga gac cag ctg tgt gtc tgg   576
204         Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
205                     180                 185                 190
206         ggt cac tgc acc aaa atg gcc acc agg ggc agc aat ggg acc atc tgt   624
207         Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
208                 195                 200                 205
209         gac aac cag agg gac tgc cag ccg ggg ctg tgc tgt gcc ttc cag aga   672
210         Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
211             210                 215                 220
212         ggc ctg ctg ttc cct gtg tgc aca ccc ctg ccc gtg gag ggc gag ctt   720
213         Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
214         225                 230                 235                 240
215         tgc cat gac ccc gcc agc cgg ctt ctg gac ctc atc acc tgg gag cta   768
216         Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
217                         245                 250                 255
218         gag cct gat gga gcc ttg gac cga tgc cct tgt gcc agt ggc ctc ctc   816
219         Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
220                     260                 265                 270
221         tgc cag ccc cac agc cac agc ctg gtg tat gtg tgc aag ccg acc ttc   864
222         Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
223                 275                 280                 285
224         gtg ggg agc cgt gac caa gat ggg gag atc ctg ctg ccc aga gag gtc   912
225         Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
226             290                 295                 300
227         ccc gat gag tat gaa gtt ggc agc ttc atg gag gag gtg cgc cag gag   960
228         Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
229         305                 310                 315                 320
230         ctg gag gac ctg gag agg agc ctg act gaa gag atg gcg ctg agg gag   1008
231         Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
232                         325                 330                 335
233         cct gcg gct gcc gcc gct gca ctg ctg gga agg gaa gag att            1050
234         Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Arg Glu Glu Ile
235                     340                 345                 350
236   <210> SEQ ID NO 4
237   <211> LENGTH: 848
238   <212> TYPE: DNA
239   <213> ORGANISM: Homo sapiens
240   <220> FEATURE:
241   <221> NAME/KEY: CDS
242   <222> LOCATION: (125)..(796)
243   <400> SEQUENCE: 4
244         gaattcggca cgagagacga cgtgctgagc tgccagctta gtggaagctc tgctctgggt 60
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

FYI

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/009,802A**

DATE: 09/13/1999
TIME: 12:48:44

Input Set: **I009802A.RAW**

e	?	Error/Warning	Original Text
90	W	"N" or "Xaa" used: Feature required	caatagaaat agctaattta tttccccang tgtgtgct
42	W	"N" or "Xaa" used: Feature required	accccatttn attctagagt cnagaacgca aggatctc
87	W	Invalid/Missing Amino Acid Numbering	